What is Claimed is:

1. An isolated polynucleotide from coryneform bacteria, containing a polynucleotide sequence coding for the eno gene and selected from the group consisting of:

a) a polynucleotide that is at least 70% identical with a polynucleotide that codes for a polypeptide containing the amino-acid sequence of SEQ ID NO:2; and

b) a polynucleotide that codes for a polypeptide containing an amino acid sequence that is at least 70 % identical with the amino-acid sequence of SEQ ID No. 2;

and in which the polypeptide exhibits the activity of the enzyme enolase.

2. The polynucleotide according to claim 1, wherein said isolated polynucleotide is a recombinant DNA replicative in coryneform bacteria.

3. The polynucleotide of claim 2, wherein L-glutamic acid is replaced in the amino acid sequence (SEQ ID NO:2) at position 223 by another proteinogenic amino acid.

4. The polynucleotide of claim 3, wherein the L-amino acid replaced in position 223 is L-lysine, as represented in SEQ ID NO:4.

5. The polynucleotide of claim 4, wherein said polynucleotide contains adenine at position 817 of the nucleotide sequence, as represented in SEQ ID NO: 3.

6. The polynucleotide of claim 1, wherein said polynucleotide is RNA.

7. The polynucleotide of claim 2, wherein said polynucleotide comprises the nucleic-acid sequence of SEQ ID NO:1.

8. The polynucleotide of claim 2, wherein said polynucleotide comprises:

(i) the nucleotide sequence shown of in SEQ ID NO:1;

(ii) a nucleotide sequence at least 70% homologous to SEQ ID NO:1 and wherein one or more of the codons in said SEQ ID NO:1 are replaced with a degenerate codon;

(iv) a nucleotide sequence at least 70% homologous to SEQ ID NO:1, wherein said nucleotide sequence comprises one or more functionally neutral sense mutations that do not alter the activity of the protein/polypeptide.

9. A corynebacteria containing the polynucleotide of any one of claims 2 to 8.

10. A method for the production an L-amino acid, comprising:

a) fermenting a coryneform bacteria that produces said L-amino acid and in which the activity of the enolase enzyme is enhanced; and

b) isolating said L-amino acid from said coryneform bacteria or from the medium used to grow said coryneform bacteria.

11. The method of claim 10, wherein said L-amino acid is L-lysine.

12. The method of claim 10, wherein the enhancement of enolase activity of step a) results from the over-expression of the eno gene.

13. The method of any one of claims claim 10-12, wherein said coryneform bacteria contain a nucleotide sequence coding for the enolase enzyme of SEQ ID NO:2 but wherein the L-glutamic acid at position 223 of SEQ ID NO:2 is replaced by another proteinogenic L-amino acid.

14. The method of claim 13, wherein said L-glutamic acid at position 223 is replaced with L-lysine.

15. The method of any one of claims 10-12, wherein said coryneform bacteria over-express one or more genes encoding enzymes used in the biosynthetic pathway of said L-amino acid.

16. The method of any one of claims 10-12, wherein the metabolic paths that reduce the formation of L-lysine in said coryneform bacteria are at least partially eliminated.

17. The method of any one of claims 10-12, wherein said coryneform bacteria are transformed with a plasmid vector comprising a nucleotide sequence coding for the eno gene.

18. The method of any one of claims 10-12, wherein said coryneform bacteria over-expresses the dapA gene coding for dihydrodipicolinate synthase.

19. The method of any one of claims 10-12, wherein said coryneform bacteria over-expresses the lysC gene coding for a feedback-resistant aspartate kinase.

20. The method of any one of claims 10-12, wherein said coryneform bacteria over-expresses the gap gene coding for glyceraldehyde-3-phosphate dehydrogenase.

21. The method of any one of claims 10-12, wherein said coryneform bacteria over-expresses the tpi gene coding for triosephosphate isomerase.

22. The method of any one of claims 10-12, wherein said coryneform bacteria over-expresses the pgk gene coding for 3-phosphoglycerate kinase.

23. The method of any one of claims 10-12, wherein said coryneform bacteria over-expresses the pyc gene coding for pyruvate carboxylase.